

Serial Number: 09/734,002

ENTERED

O/PE

#3: 0280

OHW

01/24

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Corrected invalid amino acid numbering in Seq. #2

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/734,002

DATE: 01/10/2001  
TIME: 12:26:20

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\01102001\I734002.raw

## SEQUENCE LISTING

## C--&gt; 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Motoharu SEKI et al.  
7 (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO  
9 (iii) NUMBER OF SEQUENCES: 14  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
13 (B) STREET: 2033 K Street, N.W., Suite 800  
14 (C) CITY: Washington  
15 (D) STATE: D.C.  
16 (E) COUNTRY: U.S.A.  
17 (F) ZIP: 20006  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
21 (B) COMPUTER: IBM Compatible  
22 (C) OPERATING SYSTEM: MS-DOS  
23 (D) SOFTWARE: Wordperfect 5.1  
30 (vi) CURRENT APPLICATION DATA:  
C--> 31 (A) APPLICATION NUMBER: US/09/734,002  
C--> 32 (B) FILING DATE: 12-Dec-2000  
33 (C) CLASSIFICATION:  
35 (vii) PRIOR APPLICATION DATA:  
C--> 36 (A) APPLICATION NUMBER: PCT/JP96/01956  
C--> 37 (B) FILING DATE: July 12, 1996  
C--> 39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: Lee Cheng  
41 (B) REGISTRATION NUMBER: 40,949  
42 (C) REFERENCE/DOCKET NUMBER:  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: 202-721-8200  
46 (B) TELEFAX: 202-721-8250  
47 (C) TELEX:  
49 (2) INFORMATION FOR SEQ ID NO: 1:  
51 (i) SEQUENCE CHARACTERISTICS:  
52 (A) LENGTH: 2116  
53 (B) TYPE: Nucleic acid  
54 (C) STRANDEDNESS: Double  
55 (D) TOPOLOGY: Linear  
57 (ii) MOLECULE TYPE: cDNA  
59 (vi) ORIGINAL SOURCE:  
60 (A) ORGANISM: Human  
C--> 62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
64 GGCTCCTTAC CCACCCGGAG ACTTTTTTTT GAAAGGAAAC TAGGGAGGGAGGGAGAGGGA 60  
66 GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACACTTCA CT ATG 115  
67 Met  
68 L  
70 ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTC GAT TTC GTG CAT CAT 163

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/734,002 DATE: 01/10/2001  
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Input Set : A:\Cpg.pto  
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71 Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His
72          5          10          15
74 TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA      211
75 Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr
76          20          25          30
78 GTC TGC CGA ACG GAG CAG TAT TTC AAT CTC GAG CTT TGG TTA CAA AAG      259
79 Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys
80          35          40          45
82 TAC GGC TAC CTT CCA CCG ACT GAC CCC AGA ATG TCA GTG CTG CGC TCT      307
83 Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg Ser
84 50          55          60          65
86 GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC      355
87 Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly
88          70          75          80
90 ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG      403
91 Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys
92          85          90          95
94 AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT      451
95 Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe
96          100          105          110
98 CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC      499
99 His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His
100          115          120          125
102 AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC      547
103 Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp
104 130          135          140          145
106 CGT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT CTG TCG CAG AAT      595
107 Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn
108          150          155          160
110 GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT      643
111 Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn
112          165          170          175
114 GGC AAA CGT GAT GTG GAT ATA ACC ATT ATT TTT GCA TCT GGT TTC CAT      691
115 Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe His
116          180          185          190
118 GGG GAC AGC TCT CCC TTT GAT GGA GAG GGA GGA TTT TTG GCA CAT GCC      739
119 Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His Ala
120          195          200          205
122 TAC TTC CCT GGA CCA GGA ATT GGA GGA GAT ACC CAT TTT GAC TCA GAT      787
123 Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser Asp
124 210          215          220          225
126 GAG CCA TGG ACA CTA GGA AAT CCT AAT CAT GAT GGA AAT GAC TTA TTT      835
127 Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe
128          230          235          240
130 CTT GTA GCA GTC CAT GAA CTG GGA CAT GCT CTG GGA TTG GAG CAT TCC      883
131 Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His Ser
132          245          250          255
134 AAT GAC CCC ACT GCC ATC ATG GCT CCA TTT TAC CAG TAC ATG GAA ACA      931
135 Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu Thr

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136          260          265          270
138 GAC AAC TTC AAA CTA CCT AAT GAT CAT TTA CAG GGC ATC CAG AAA ATA      979
139 Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys Ile
140          275          280          285
142 TAT GGT CGA CCT GAC AAG ATT CCT CCA CCT ACA AGA CCT CTA CCG ACA      1027
143 Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr
144 290          295          300          305
146 GTG CCC CCA CAC CGC TCT ATT CCT CCG GCT GAC CCA AGG AAA AAT GAC      1075
147 Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp
148          310          315          320
150 AGG CCA AAA CCT CCT CGG CCT CCA ACC GGC AGA CCC TCC TAT CCC GGA      1123
151 Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly
152          325          330          335
154 GCC AAA CCC AAC ATC TGT GAT CGG AAC TTT AAC ACT CTA GCT ATT CTT      1171
155 Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu
156          340          345          350
158 CGT CGT GAG ATG TTT GTT TTC AAG GAC CAG TGG TTT TGG CGA GTG AGA      1219
159 Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg
160          355          360          365
162 AAC AAC AGG GTG ATG GAT GGA TAC CCA ATG CAA ATT ACT TAC TTC TGG      1267
163 Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp
164 370          375          380          385
166 CGG GGC TTG CCT CCT AGT ATC GAT GCA GTT TAT GAA AAT AGC GAC GGG      1315
167 Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly
168          390          395          400
170 AAT TTT GTG TTC TTT AAA GGT AAC AAA TAT TGG GTG TTC AAG GAT ACA      1363
171 Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp Thr
172          405          410          415
174 ACT CTT CAA CCT GGT TAC CCT CAT GAC TTG ATA ACC CTT CGA AGT GGA      1411
175 Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser Gly
176          420          425          430
178 ATT CCC CCT CAT GGT ATT GAT TCA GCC ATT TGG TGG GAG GAC GTC GGG      1459
179 Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val Gly
180          435          440          445
182 AAA ACC TAT TTC TTC AAG GGA GAC AGA TAT TGG AGA TAT AGT GAA GAA      1507
183 Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu Glu
184 450          455          460          465
186 ATG AAA ACA ATG GAC CCT GGC TAT CCC AAG CCA ATC ACA GTC TGG AAA      1555
187 Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp Lys
188          470          475          480
190 GGG ATC CCT GAA TCT CCT CAG GGA GCA TTT GTA CAC AAA GAA AAT GGC      1603
191 Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn Gly
192          485          490          495
194 TTT ACG TAT TTC TAC AAA GGA AAG GAG TAT TGG AAA TTC AAC AAC CAG      1651
195 Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn Gln
196          500          505          510
198 ATA CTC AAG GTA GAA CCT GGA CAT CCA AGA TCC ATC CTC AAG GAT TTT      1699
199 Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp Phe
200          515          520          525

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Input Set : A:\Cpg.pto

Output Set: N:\CRF3\01102001\I734002.raw

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202 ATG GGC TGT GAT GGA CCA ACA GAC AGA GTT AAA GAA GGA CAC AGC CCA 1747
203 Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser Pro
204 530 535 540 545
206 CCA GAT GAT GTA GAC ATT GTC ATC AAA CTG GAC AAC ACA GCC AGC ACT 1795
207 Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser Thr
208 550 555 560
210 GTG AAA GCC ATA GCT ATT GTC ATT CCC TGC ATC TTG GCC TTA TGC CTC 1843
211 Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu
212 565 570 575
214 CTT GTA TTG GTT TAC ACT GTG TTC CAG TTC AAG AGG AAA GGA ACA CCC 1891
215 Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro
216 580 585 590
218 CGC CAC ATA CTG TAC TGT AAA CGC TCT ATG CAA GAG TGG GTG TGA TGTAGG 1942
219 Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val
220 595 600 605
221 GTTTTTCTT CTTTCTTCT TTTGCAGGAG TTTGTGGTAA CTTGAGATTC AAGACAAGAG 2002
223 CTGTTATGCT GTTTCCTAGC TAGGAGCAGG CTGTGGGCAG CCTGATTCGG GGCTGACCTT 2062
225 TCAAACCAGA GGGTTGCTGG TCCTGCACAT GAGTGGAAAT ACACATCATGG GGAA 2116
229 (2) INFORMATION FOR SEQ ID NO: 2:
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 607
233 (B) TYPE: Amino acid
234 (C) STRANDEDNESS: Single
235 (D) TOPOLOGY: Linear
237 (ii) MOLECULE TYPE: Protein
239 (vi) ORIGINAL SOURCE:
240 (A) ORGANISM: Human
C--> 242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
244 Met Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His
245 1 5 10 15
247 His Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala
248 20 25 30
250 Thr Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln
251 35 40 45
253 Lys Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg
254 50 55 60
256 Ser Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr
257 65 70 75 80
259 Gly Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met
260 85 90 95
262 Lys Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys
263 100 105 110
265 Phe His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln
266 115 120 125
268 His Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly
269 130 135 140
271 Asp Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln
272 145 150 155 160
274 Asn Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu

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Input Set : A:\Cpg.pto

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275      165      170      175
277 Asn Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe
278      180      185      190
280 His Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His
281      195      200      205
283 Ala Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser
284      210      215      220
286 Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu
287 225      230      235      240
289 Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His
290      245      250      255
292 Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu
293      260      265      270
295 Thr Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys
296      275      280      285
298 Ile Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro
299      290      295      300
301 Thr Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn
302 305      310      315      320
304 Asp Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro
305      325      330      335
307 Gly Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile
308      340      345      350
310 Leu Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val
311      355      360      365
313 Arg Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe
314      370      375      380
316 Trp Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp
317 385      390      395      400
319 Gly Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp
320      405      410      415
322 Thr Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser
323      420      425      430
325 Gly Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val
326      435      440      445
328 Gly Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu
329      450      455      460
331 Glu Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp
332 465      470      475      480
334 Lys Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn
335      485      490      495
337 Gly Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn
338      500      505      510
340 Gln Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp
341      515      520      525
343 Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser
344      530      535      540
346 Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser
347 545      550      555      560

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## VERIFICATION SUMMARY

DATE: 01/10/2001

PATENT APPLICATION: US/09/734,002

TIME: 12:26:21

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\01102001\I734002.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
 L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:39 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
 L:36 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:  
 L:37 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:  
 L:62 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:242 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:370 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:386 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:401 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:416 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:432 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:446 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]  
 L:447 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
 L:451 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:462 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]  
 L:463 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
 L:467 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:478 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]  
 L:479 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
 L:483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:494 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]  
 L:495 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
 L:499 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:510 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]  
 L:511 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
 L:515 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:531 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:550 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14